

**Appl. No. : Not Yet Assigned**  
**Filed : October 13, 2005**

**AMENDMENTS TO THE CLAIMS**

**Please cancel Claims 1-22, without prejudice or disclaimer.**

**Please add Claims 23-48.**

23. (New) A method of making a single stranded nucleic acid molecule comprising:
- (a) providing a first oligonucleotide;
  - (b) providing a second oligonucleotide;
  - (c) annealing a first adaptor oligonucleotide to said first and said second oligonucleotide, wherein the 5' terminus of said adaptor oligonucleotide is complementary to the 5' terminus of said first oligonucleotide and the 3' terminus of said adaptor oligonucleotide is complementary to the 3' terminus of said second oligonucleotide;
  - (d) ligating said first and second oligonucleotides; and
  - (e) removing said adaptor oligonucleotide.
24. (New) The method of Claim 23, further comprising the step of annealing a second adaptor oligonucleotide to the free termini of said first or second oligonucleotides.
25. (New) The method of Claim 24, further comprising the step of annealing a third oligonucleotide to said second adaptor oligonucleotide.
26. (New) The method of Claim 23, further comprising the step of filling in a gap between the neighboring ends of said first and second oligonucleotides.
27. (New) The method of Claim 23, wherein said adaptor oligonucleotide comprises at least four consecutive nucleotides that are complementary to said first and said second oligonucleotides.
28. (New) The method of Claim 23, wherein said annealing and ligating steps are simultaneous.
29. (New) The method of Claim 27, wherein said annealing and ligating steps are simultaneous.
30. (New) The method of Claim 23, wherein said first adaptor is provided in molar excess of said first or second oligonucleotides.

31. (New) The method of Claim 23, wherein said single stranded nucleic acid is a member of a collection of single stranded nucleic acids and either said first or second oligonucleotide is invariable in sequence between all members of said collection.

32. (New) The method of Claim 31, wherein either said first or said second oligonucleotide, which is not invariable, is variable in sequence between different members of said collection.

33. (New) The method of Claim 31, wherein said oligonucleotides are variable in sequence between different members of said collection of nucleic acid molecules.

34. (New) The method of Claim 32, wherein the oligonucleotide comprising a variable sequence is in molar excess over said oligonucleotide that comprises an invariable sequence.

35. (New) The method of Claim 32, wherein the 5' or 3' termini of said oligonucleotide that is variable in sequence, which anneal to said 5' or 3' termini of said adaptor oligonucleotide, are invariable between different members of said oligonucleotides of variable sequences.

36. (New) The method of Claim 23, wherein said ligating step comprises T4 DNA ligase.

37. (New) The method of Claim 23, wherein said ligating step comprises 5% polyethylene glycol.

38. (New) The method of Claim 23, wherein said ligating step comprises 15% polyethylene glycol.

39. (New) The method of Claim 23, wherein said ligating step comprises polyethylene glycol 6000.

40. (New) The method of Claim 23, wherein said ligating step comprises reacting about 1 unit of T4 DNA ligase with about 4 pmol of termini of said oligonucleotides that are annealed to said adaptor oligonucleotide.

41. (New) The method of Claim 23, further comprising purifying said single stranded nucleic acid molecules.

42. (New) The method of Claim 41, wherein said purifying step comprises PAGE electrophoresis, HPLC, or chromatography.

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43. (New) The method of Claim 23, further comprising modifying at least one oligonucleotide.

44. (New) The method of Claim 23, wherein at least one oligonucleotide is modified.

45. (New) The method of Claim 44, wherein said modification is a ribonucleotide, a spacer, or a nucleotide comprising a detectable label.

46. (New) The method of Claim 31, wherein said oligonucleotide comprising an invariable sequence is modified.

47. (New) The method of Claim 31, further comprising the identification of an SNP.

48. (New) The method of Claim 31, wherein said members of said collection of nucleic acid molecules are used in a ligase-independent cloning or two-step PCR.